

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:45:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173916.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10173916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173916_1.fastq.gz SRR10173916_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:45:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,342,342
Mapped reads	2,278,970 / 97.29%
Unmapped reads	63,372 / 2.71%
Mapped paired reads	2,278,970 / 97.29%
Mapped reads, first in pair	1,141,573 / 48.74%
Mapped reads, second in pair	1,137,397 / 48.56%
Mapped reads, both in pair	2,235,810 / 95.45%
Mapped reads, singletons	43,160 / 1.84%
Secondary alignments	0
Supplementary alignments	230,137 / 9.83%
Read min/max/mean length	30 / 133 / 128.34
Duplicated reads (estimated)	1,758,528 / 75.08%
Duplication rate	64.36%
Clipped reads	931,008 / 39.75%

2.2. ACGT Content

Number/percentage of A's	80,831,207 / 29.99%
Number/percentage of C's	52,925,022 / 19.64%
Number/percentage of T's	80,783,994 / 29.97%
Number/percentage of G's	54,964,225 / 20.39%
Number/percentage of N's	2,949 / 0%

GC Percentage	40.03%
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2.3. Coverage

Mean	0.0871
Standard Deviation	1.455

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	918,659.06
Standard Deviation	9,004,046.77
P25/Median/P75	146 / 203 / 291

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	2,769,401
Insertions	27,369
Mapped reads with at least one insertion	1.17%
Deletions	60,679
Mapped reads with at least one deletion	2.6%
Homopolymer indels	43.05%

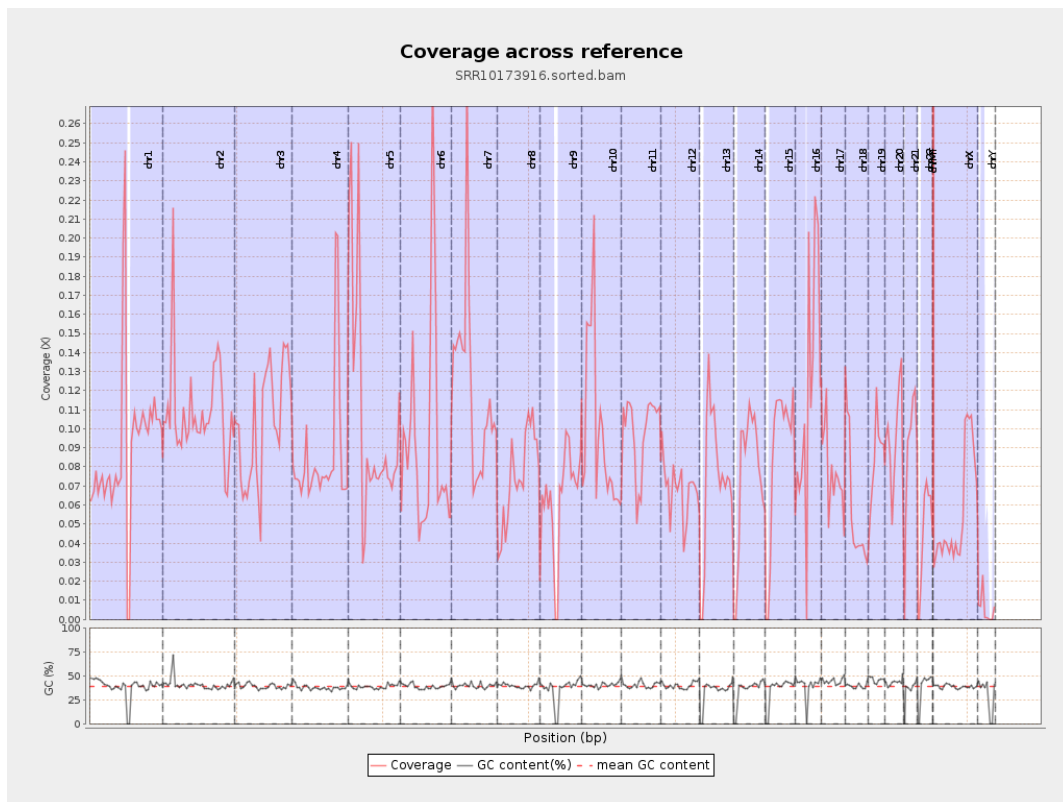
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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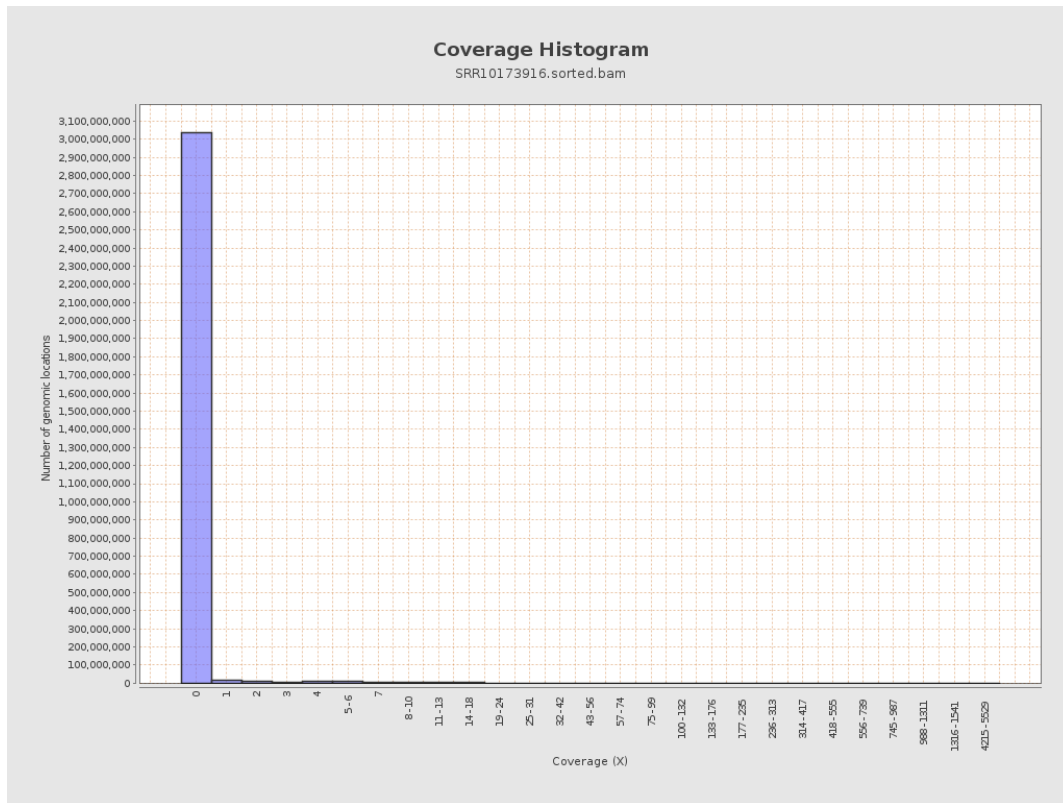
		bases	coverage	deviation
chr1	249250621	22398736	0.0899	1.311
chr2	243199373	26403768	0.1086	3.9332
chr3	198022430	20290359	0.1025	0.9158
chr4	191154276	16480423	0.0862	0.8913
chr5	180915260	19085736	0.1055	0.9312
chr6	171115067	15630886	0.0913	0.8733
chr7	159138663	19223571	0.1208	1.3971
chr8	146364022	10983870	0.075	0.8129
chr9	141213431	9134240	0.0647	0.7838
chr10	135534747	13209883	0.0975	1.3943
chr11	135006516	13251376	0.0982	0.9082
chr12	133851895	9229541	0.069	0.7418
chr13	115169878	8495882	0.0738	0.7796
chr14	107349540	8245713	0.0768	0.783
chr15	102531392	8796150	0.0858	0.8268
chr16	90354753	10576191	0.1171	1.1516
chr17	81195210	6303255	0.0776	0.8191
chr18	78077248	4451090	0.057	1.1066
chr19	59128983	4984080	0.0843	1.2859
chr20	63025520	6115203	0.097	0.8735
chr21	48129895	4192074	0.0871	0.8504
chr22	51304566	2344291	0.0457	0.5706
chrMT	16571	796712	48.0787	40.5816
chrX	155270560	8690755	0.056	0.6728

chrY	59373566	339008	0.0057	0.2693
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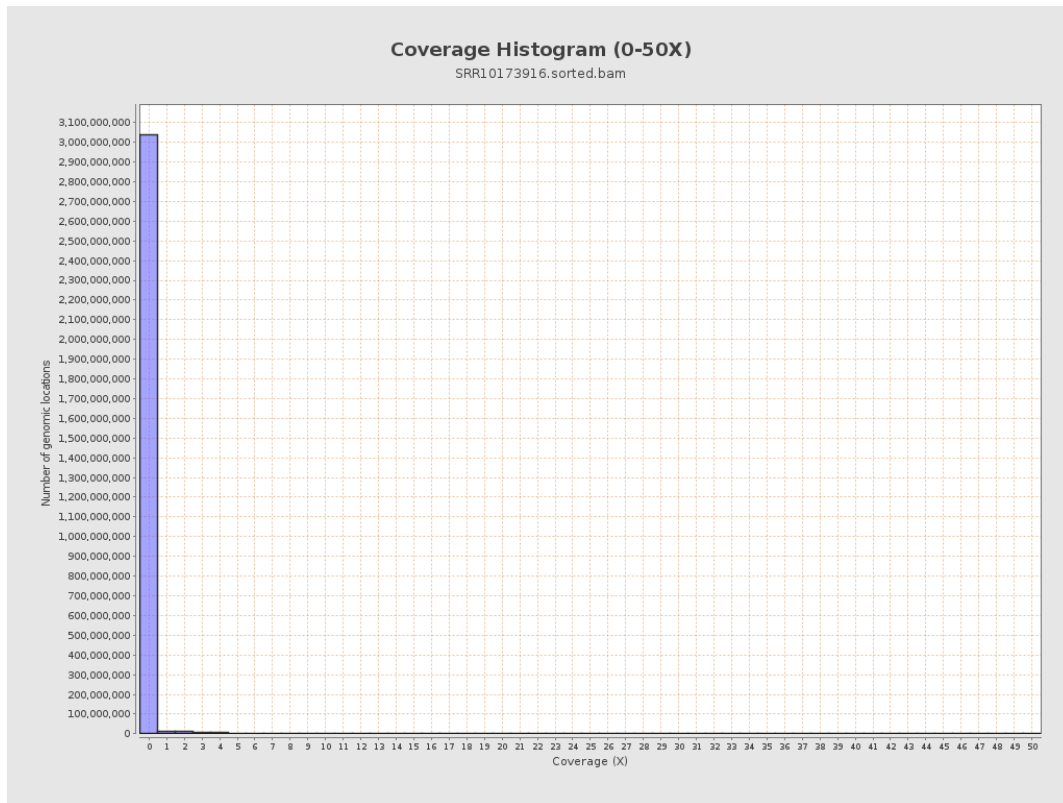
3. Results : Coverage across reference



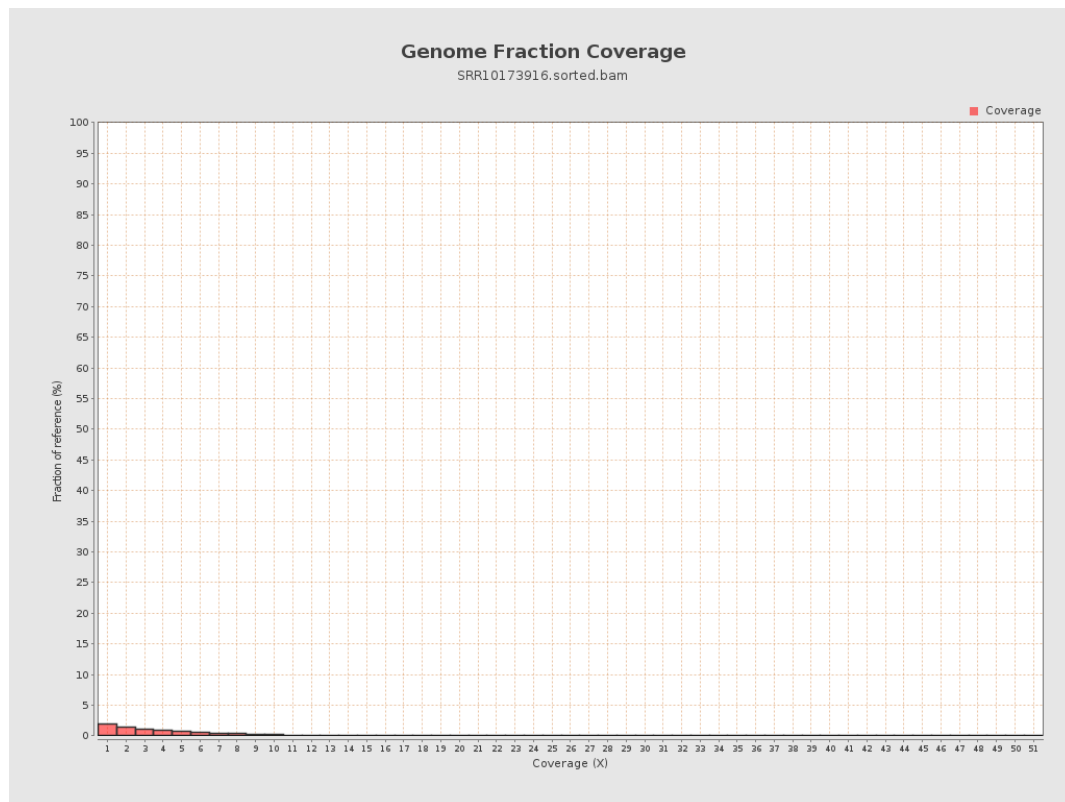
4. Results : Coverage Histogram



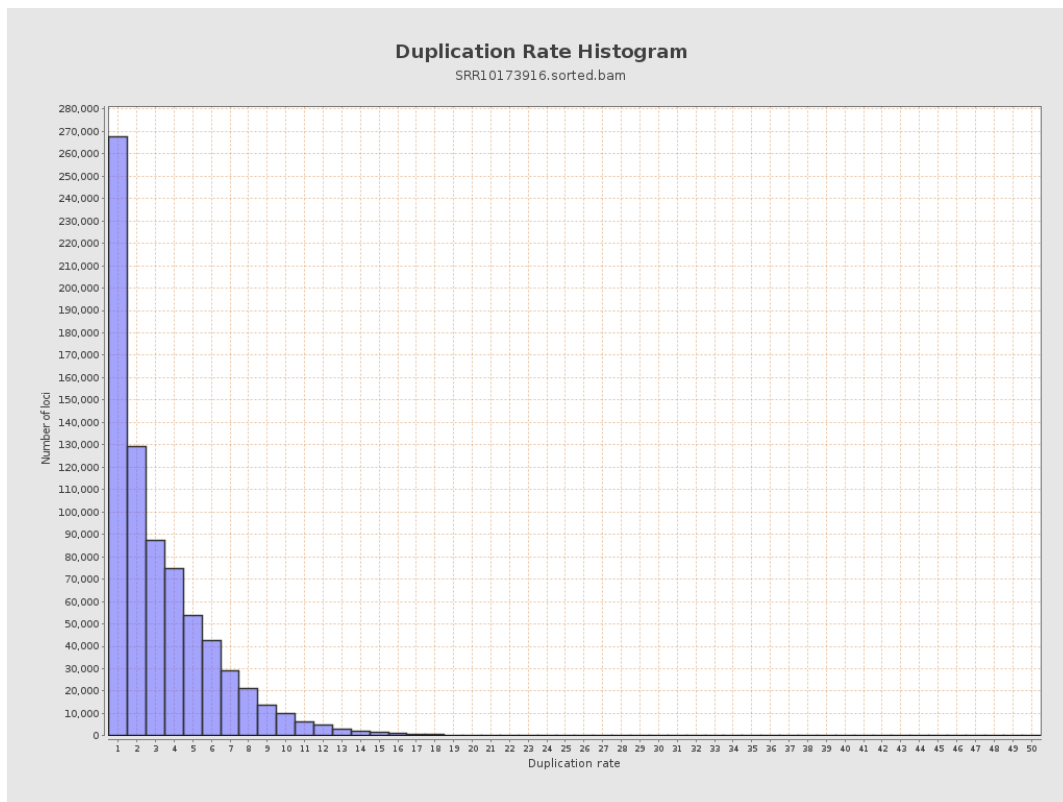
5. Results : Coverage Histogram (0-50X)



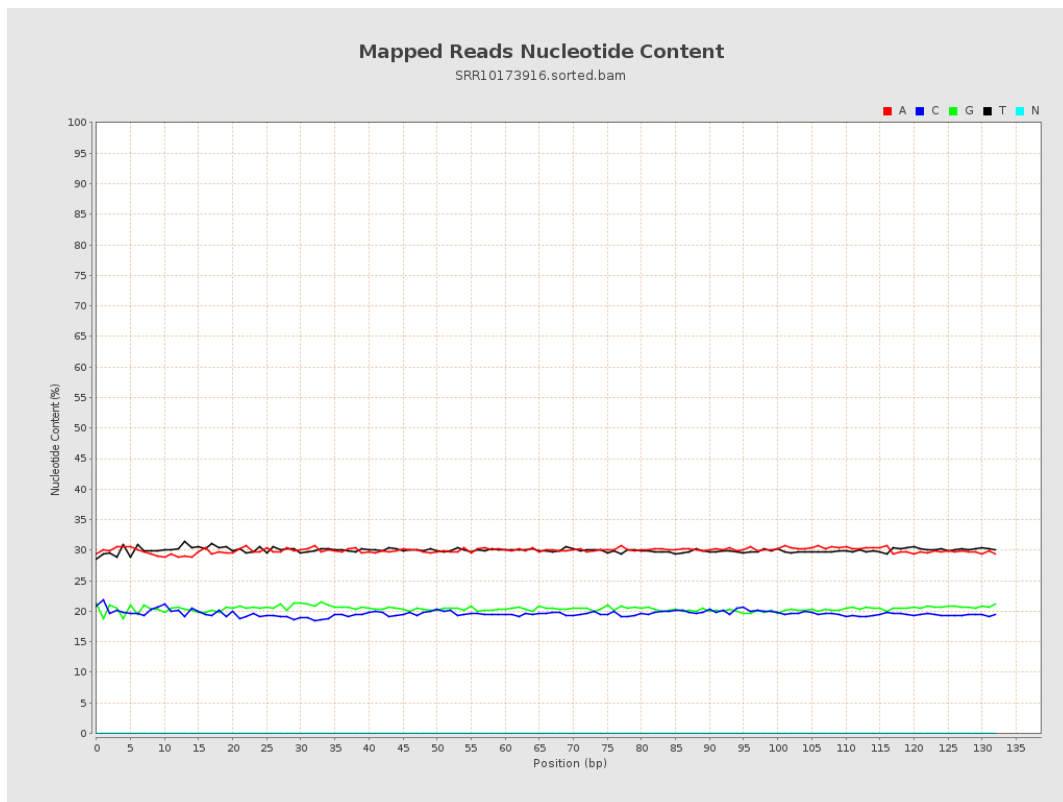
6. Results : Genome Fraction Coverage



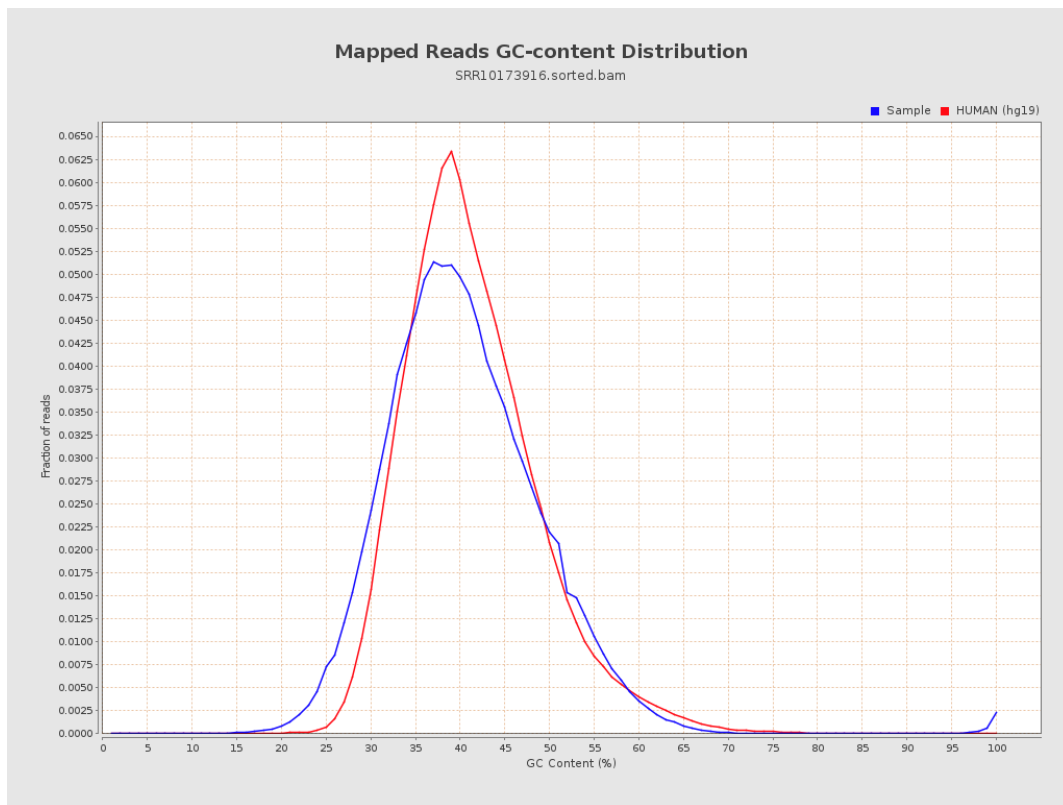
7. Results : Duplication Rate Histogram



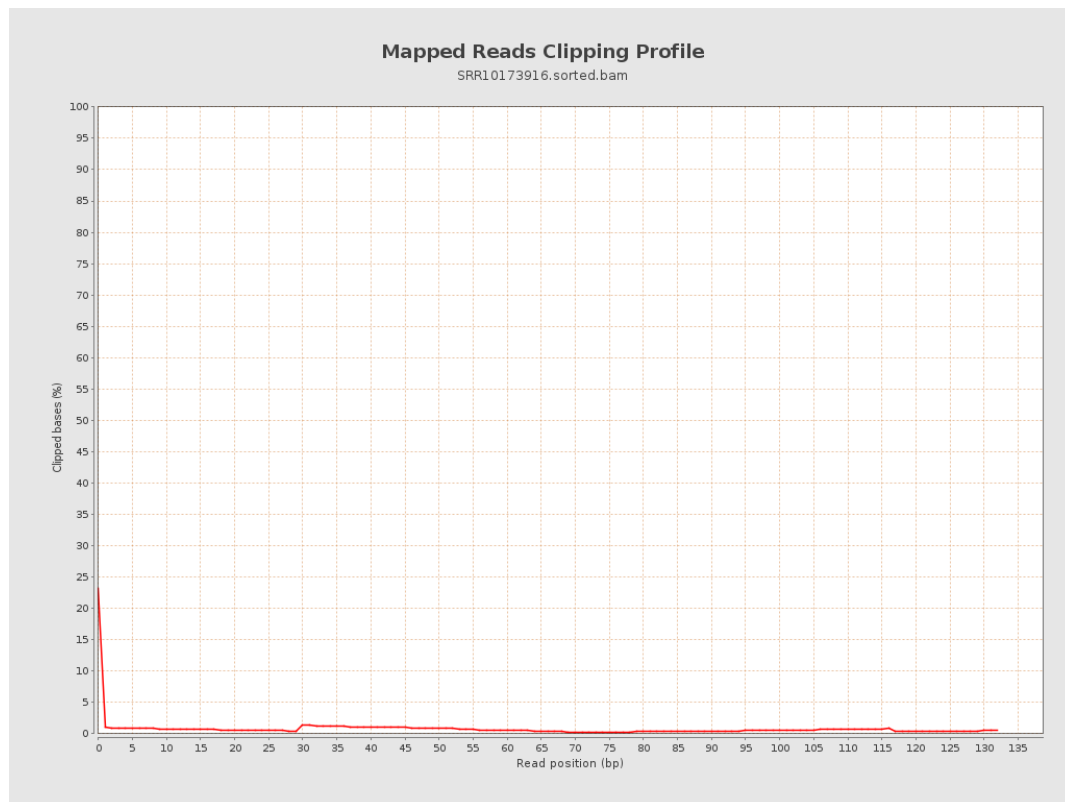
8. Results : Mapped Reads Nucleotide Content



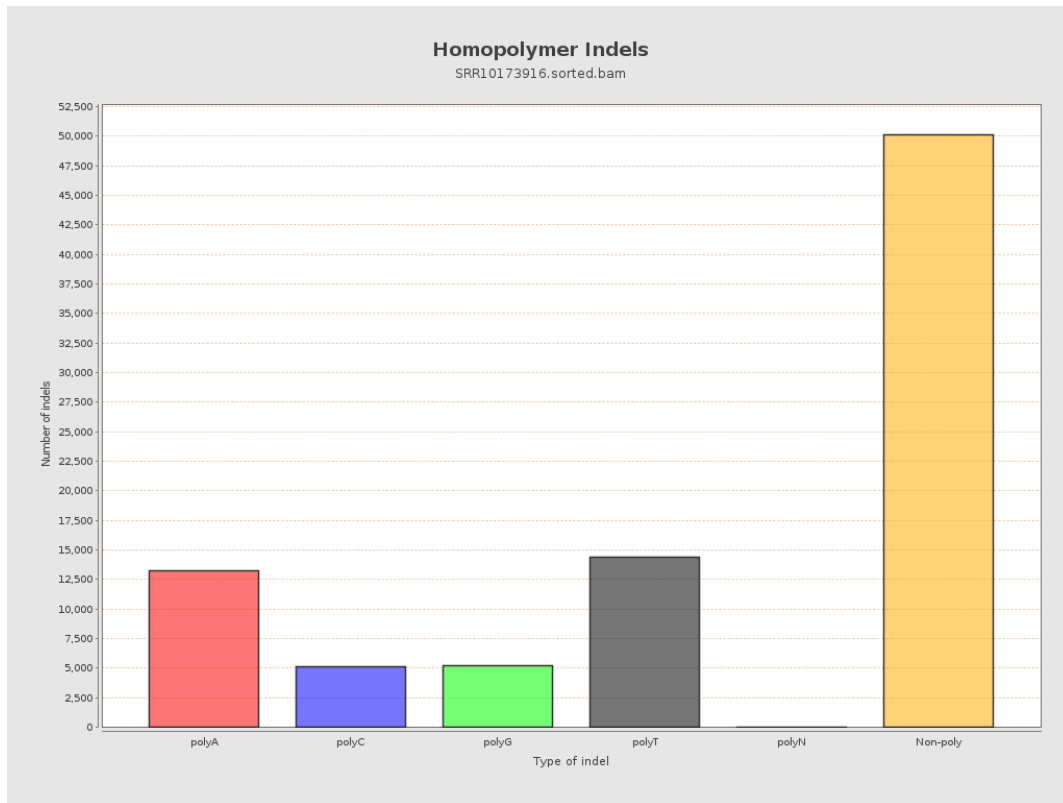
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



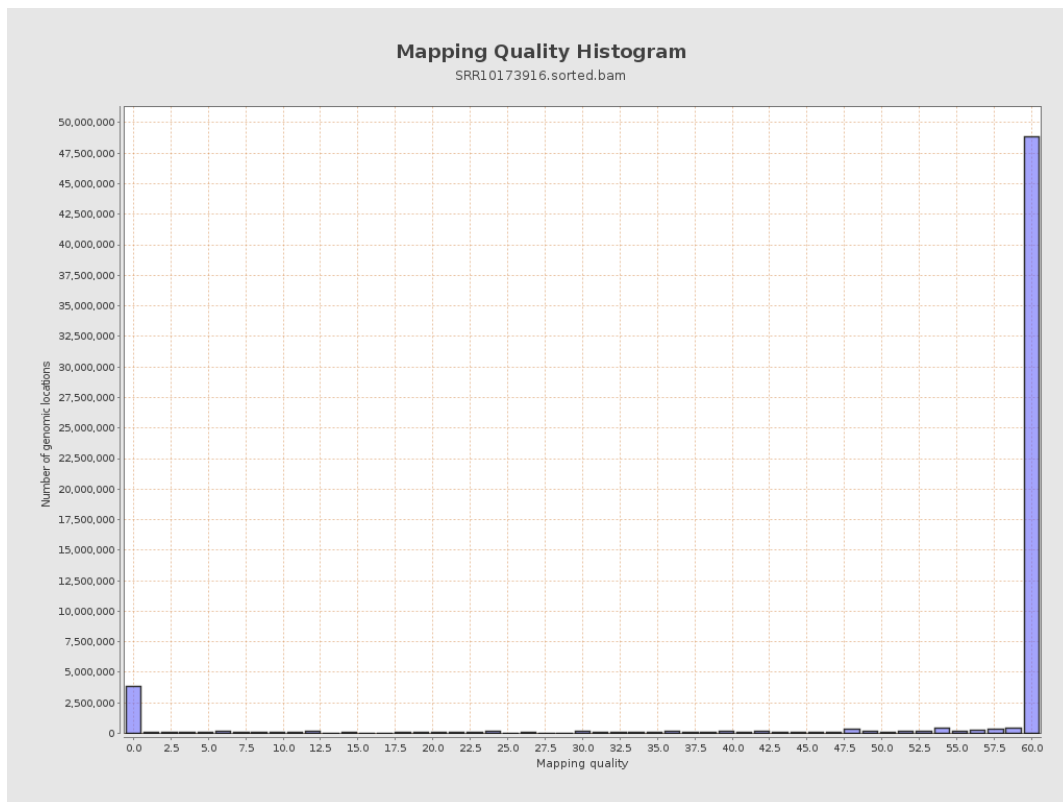
11. Results : Homopolymer Indels



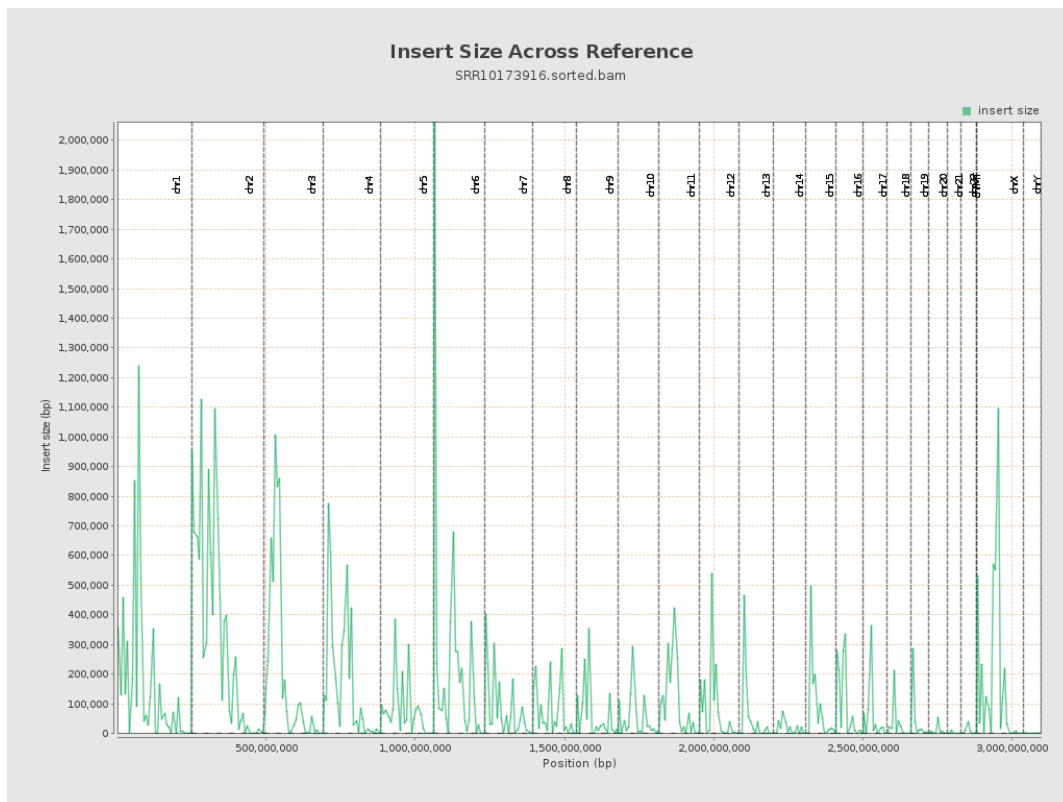
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

